

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

20. (CURRENTLY AMENDED) A computer mediated method of identifying DNA sequences that control the expression of different collections of genes in a genome comprising detecting, by computer, one or more pairs of first and second non-adjacent DNA sequence data which
5 represents a DNA molecule that could bind to one RNA molecule such that a first RNA sequence in that RNA molecule can bind to a first non-adjacent DNA sequence data and a second RNA sequence data in that RNA molecule can bind to a second non-adjacent DNA sequence, ~~where the DNA sequence data and the RNA molecule can form a~~
10 ~~tetradic relationship such that T1=C1 and T2=C2 where T1 and T2 are DNA sequences, where the C1 sequence is adjacent to the C2 sequence, where the T1 and T2 sequences of data are on the same chromosome, and where the C1/C2 sequence data are on the same~~
15 ~~chromosome as T1 and T2 or where the C1/C2 sequence data are on a chromosome different from T1 and T2 and outputting the results thereof to a utilization facility.~~

21. (PREVIOUSLY PRESENTED) A computer mediated method of identifying DNA sequences that control the expression of different collections of genes in a genome comprising, by computer, detecting, changes in connectron behavior in the genome as a
5 function of changes in the sequence of the genome and outputting the results thereof to a utilization facility.

22. (PREVIOUSLY PRESENTED) A computer mediated method of detecting changes in expression of different gene collections in a genome, comprising: by computer, detecting changes in expression of different gene collections in a genome that result in changes in

5 the level of connectron control sequences caused by a stimulus and outputting the results thereof to a utilization facility.

23. (PREVIOUSLY PRESENTED) A computer mediated method of detecting, by computer, where and when new genes have been integrated into a host genome comprising detecting an operable link between a newly introduced gene and a preexisting connectron behavior in said host genome and outputting the results thereof to a utilization facility.

24. (PREVIOUSLY PRESENTED) A computer mediated method of detecting the expression effect of different gene collections in a given host genome, comprising: by computer, detecting the effect of connectrons on transcription and outputting the results thereof to a utilization facility.

25. (PREVIOUSLY PRESENTED) A computer mediated method of changing the expression of different gene collections in a genome comprising modifying, by a computer, identification of connectron organization and outputting the results thereof to a utilization facility.

26. (PREVIOUSLY PRESENTED) A method of detecting connectron control and target sequences in a given genome comprising:

by computer:

5 determining the base composition of said genome,
determining one or more sites of control sequence organization, and/or
determining one or more sites of target application and outputting the results thereof to a utilization facility.

27. (PREVIOUSLY PRESENTED) A computer mediated method of determining the response of a cell in any tissue to changes in the cell's environment and/or genetic composition comprising: by computer, providing a complete genomic DNA sequence for the organism determining the effect of changes in connectrons due to application of a given stimulus to the genome and outputting the results thereof to a utilization facility.

28. (CURRENTLY AMENDED) The method as defined in claim 20, when applied to prokaryotes, archaea, single-celled eukaryotes and multi-celled eukaryotes, where the DNA sequence and the RNA molecule can form a tetradic relationship such that T1-C1 and T2-C2 where T1 and T2 are DNA sequences 20 or more bases in length, where the C1 sequence is adjacent to the C2 sequence, where the T1 and T2 sequences are on the same chromosome, and where the C1/C2 sequences are on the same chromosome as T1 and T2 or where the C1/C2 sequences are on a chromosome different from T1 and T2, determines connectrons wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2

sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

25 T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

29. (PREVIOUSLY PRESENTED) The method as defined in claim 20, when applied to prokaryotes, archaea, single-celled eukaryotes and multi-celled eukaryotes, where the DNA sequences and the RNA molecule function as a connectron that permits many different C1/C2 short loops to control the existence of a T1-T2 long loop and wherein said C1/C2 short loops can be on the same chromosome or on different chromosomes from the T1-T2 long loop, determines connectrons wherein:

10 C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

15 C1/C2 - any positive or negative strand DNA sequence of 540 or more bases such that the C1 sequence is adjacent to the C2 sequence,

20 T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

30. (PREVIOUSLY PRESENTED) The method as defined in claim 20, when applied to prokaryotes, archaea, single-celled eukaryotes and multi-celled eukaryotes, where the DNA sequences and the RNA molecule function as a connectron that permits one C1/C2 short loop to control the existence of many T1-T2 long loops, the C1/C2 short loop can be on the same chromosome or on different chromosomes from the T1-T2 long loops, determines connectrons wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1

sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

31. (PREVIOUSLY PRESENTED) The method as defined in claim 20, when applied to where the DNA sequences and the RNA molecule function as a connectron between prokaryotes and their plasmids and wherein said connectron implements a control mechanism between the two genomes that makes it possible from them to form a symbiotic relationship, and in the case of D. radiodurans the relationship is not symmetric, and the D. radiodurans genome sends C1/C2 short loops to the MP1 plasmid, determines connectrons wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

32. (PREVIOUSLY PRESENTED) The method as defined in claim 20, where the DNA sequences and the RNA molecule function as a connectron that exist in a plant or a higher animal.

33. (PREVIOUSLY PRESENTED) The method as defined in claim 20, when applied to prokaryotes, archaea, single-celled eukaryotes and multi-celled eukaryotes, where the DNA sequences and the RNA molecule function as a connectron that permits one C1/C2 short loop to control the existence of one or more T1-T2 long loops without being subject to any expression controls other than those of the gene to which the C1/C2 is 3'UTR, determines connectrons wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart,

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart, and

3'UTR - untranslated 3' end of an mRNA is beyond the end of the last exon, a stop codon in the mRNA causes the ribosome to stop the translation of mRNA into protein.

34. (PREVIOUSLY PRESENTED) The method as defined in claim 20, when applied to prokaryotes, archaea, single-celled eukaryotes and multi-celled eukaryotes, where the DNA sequences and the RNA molecule function as a connectron that permits one C1/C2 short loop to control the existence of one or more T1-T2 long loops such that this C1/C2 short loop is itself subject to expression control by another T1-T2 long loop which surrounds it, determines connectrons wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1

sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

35. (PREVIOUSLY PRESENTED) The method as defined in claim 20, when applied to prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes, where the DNA sequences and the RNA molecule function as a connectron that permits one C1/C2 short loop to control the existence of the T1-T2 long loop that surrounds it, determines connectrons wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 50 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

36. (PREVIOUSLY PRESENTED) The method as defined in claim 20, where the DNA sequences and the RNA molecule function as a connectron that does not have any genes within the T1-T2 long loop, determines connectrons wherein:

5 T1 sequence is any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, and

10 T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, and the T2 or T1 sequences must be between about 1kb and 105kb apart.

37. (PREVIOUSLY PRESENTED) The method as defined in claim 20, where the DNA sequences and the RNA molecule function as a geneless connectron where one C1/C2 short loop controls the existence of many geneless T1-T2 long loops, determines connectrons wherein:

5 C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

10 C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

15 T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2

sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

20